SEQUENCE LISTING

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       Hueckelhoven, Ralph

<120> METHOD FOR INCREASING RESISTANCE AGAINST STRESS FACTORS IN PLANTS

<130> 12810-00137-US

<150> PCT/EP2004/002436
<151> 2004-03-10

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<151> 2003-03-12

<160> 63

<170> PatentIn version 3.3

<210> 1
<211> 744
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(741)
<223> coding for BI1-protein

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Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
  1   5   10   15

cac gac tcc ctc aag aac ttc cgc cag atc tcc ccc gcc gtg cag tcc   96
His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser
              20   25   30

cac ctc aag ctc gtt tac ctg act cta tgc ttt gca ctg gcc tca tct   144
His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
          35   40   45

gcc gtg ggt gct tac cta cac att gcc ctg aac atc ggc ggg atg ctg   192
Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
      50   55   60

aca atg ctc gct tgt gtc gga act atc gcc tgg atg ttc tcg gtg cca   240
Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
 65   70   75   80

gtc tat gag gag agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc   288
Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
                  85   90   95

ctg gaa ggg gct tcg gtt gga cct ctg att gag ctt gcc ata gac ttt   336
Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe

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                100                    105                    110

gac cca agc atc ctc gtg aca ggg ttt gtc gga acc gcc atc gcc ttt      384
Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
        115                    120                    125

ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg      432
Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
        130                    135                    140

tac ctc ggt ggc ctg ctc tcg tct ggc ctg tcg atc ctg ctc tgg ctg      480
Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
145                    150                    155                    160

cag ttt gtc acg tcc atc ttt ggc cac tcc tct ggc agc ttc atg ttt      528
Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
                165                    170                    175

gag gtt tac ttt ggc ctg ttg atc ttc ctg ggg tac atg gtg tac gac      576
Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
                180                    185                    190

acg cag gag atc atc gag agg gcg cac cat ggc gac atg gac tac atc      624
Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
        195                    200                    205

aag cac gcc ctc acc ctc ttc acc gac ttt gtt gcc gtc ctc gtc cga      672
Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
        210                    215                    220

gtc ctc atc atc atg ctc aag aac gca ggc gac aag tcg gag gac aag      720
Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
225                    230                    235                    240

aag aag agg aag agg ggg tcc tga                                      744
Lys Lys Arg Lys Arg Gly Ser
                245
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<210> 2
<211> 247
<212> PRT
<213> Hordeum vulgare

<400> 2
Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
 1               5                   10                  15

His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser
            20                  25                  30

His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
            35                  40                  45

Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
        50                  55                  60
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Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
 65                  70                  75                  80

Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
                 85                  90                  95

Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
             100                 105                 110

Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
         115                 120                 125

Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
     130                 135                 140

Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
145                 150                 155                 160

Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
             165                 170                 175

Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
             180                 185                 190

Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
         195                 200                 205

Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
     210                 215                 220

Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
225                 230                 235                 240

Lys Lys Arg Lys Arg Gly Ser
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<210> 3
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<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(741)
<223> coding for BI1-protein

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Met Asp Ala Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
  1               5                  10                  15

tgg agc tat gat tct ctt aaa aac ttc cgt cag att tct cca gcc gtt    96
Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val
             20                  25                  30

cag aat cat ctt aaa cgg gtt tat ttg acc tta tgt tgt gct ctt gtg   144
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Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
        35                  40                  45

gcg tct gcc ttt gga gct tac ctc cat gtg ctc tgg aat atc ggc ggt   192
Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
        50                  55                  60

att ctt aca acg att gga tgt att gga act atg att tgg ctc ctt tca   240
Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser
 65                  70                  75                  80

tgt cct cct tat gaa cac caa aaa agg ctt tct ctt ctg ttt gtg tct   288
Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser
                85                  90                  95

gct gtt ctt gaa ggt gct tct gtt ggc ccc ttg atc aaa gtg gca att   336
Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile
            100                 105                 110

gat gtt gac cca agc atc ctt atc act gca ttt gtt gga act gcg ata   384
Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
            115                 120                 125

gcg ttt gtc tgt ttc tca gca gca gca atg tta gca aga cgc agg gag   432
Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
            130                 135                 140

tat ctc tac ctt gga gga ctg ctt tca tct ggc ttg tct atg cta atg   480
Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
145                 150                 155                 160

tgg ctc cag ttt gcc tct tca atc ttt ggt ggc tct gca tct atc ttt   528
Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
                165                 170                 175

aag ttt gag ttg tac ttt gga ctt ttg atc ttt gtg gga tac atg gtg   576
Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
            180                 185                 190

gtg gac aca caa gag att ata gaa aag gca cac ctc ggt gac atg gac   624
Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
            195                 200                 205

tat gta aaa cat tcg ttg acc ctt ttc act gac ttt gta gct gtg ttt   672
Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
    210                 215                 220

gtt cgg att ctc atc ata atg ttg aag aac tca gca gat aaa gaa gag   720
Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
225                 230                 235                 240

aag aag aag aaa agg aga aac tgaggggatg taaagtaaat ttaactttat     771
Lys Lys Lys Lys Arg Arg Asn
                245

ggttgttatc gtgtgtggcc actttgaaga tattacttgt tagcactctc tattggtgac 831
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cagacatgtt ccactaaaaa aggatctgct tgtttcactt ctgcacaagt accatcttca 891

gattgtaaat gactcgagtg ttgttcttct tttcataaac ttttgttctt taagagtttg 951

gttctactga ttgcatctta ccaagctaag aataatgtag gaaaatgata atcctgttta 1011

aattttctaa aatgtgtgca tttcagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa   1067

<210> 4
<211> 247
<212> PRT
<213> Arabidopsis thaliana

<400> 4
Met Asp Ala Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
  1   5   10   15

Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val
             20   25   30

Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
         35   40   45

Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
     50   55   60

Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser
 65   70   75   80

Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser
             85   90   95

Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile
         100   105   110

Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
         115   120   125

Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
     130   135   140

Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
145   150   155   160

Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
             165   170   175

Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
             180   185   190

Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
         195   200   205

Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
     210   215   220

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Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
225             230         235             240

Lys Lys Lys Lys Arg Arg Asn
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<210> 5
<211> 1160
<212> DNA
<213> Nicotiana tabacum

<220>
<221> CDS
<222> (1)..(747)
<223> coding for BI1-protein

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atg gag tct tgc aca tcg ttc ttc aat tca cag tcg gcg tcg tct cgc    48
Met Glu Ser Cys Thr Ser Phe Phe Asn Ser Gln Ser Ala Ser Ser Arg
  1             5                  10                  15

aat cgc tgg agt tac gat tct ctt aag aac ttc cgc cag atc tct ccc    96
Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro
             20                  25                  30

ttt gtt caa act cat ctc aaa aag gtc tac ctt tca tta tgt tgt gct   144
Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala
         35                  40                  45

tta gtt gct tcg gct gct gga gct tac ctt cac att ctt tgg aac att   192
Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
     50                  55                  60

ggt ggc tta ctt acg aca ttg gga tgt gtg gga agc ata gtg tgg ctg   240
Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
 65                  70                  75                  80

atg gcg aca cct ctg tat gaa gag caa aag agg ata gca ctt ctg atg   288
Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
                 85                  90                  95

gca gct gca ctg ttt aaa gga gca tct att ggt cca ctg att gaa ttg   336
Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
                100                 105                 110

gct att gac ttt gac cca agc att gtg atc ggt gct ttt gtt ggt tgt   384
Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
            115                 120                 125

gct gtg gct ttt ggt tgc ttc tca gct gct gcc atg gtg gca agg cgc   432
Ala Val Ala Phe Gly Cys Phe Ser Ala Ala Ala Met Val Ala Arg Arg
        130                 135                 140

aga gag tac ttg tat ctt gga ggt ctt ctt tca tct ggt ctc tct atc   480
Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
145                 150                 155                 160
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ctt ttc tgg ttg cac ttc gcg tcc tcc att ttt ggt ggt tct atg gcc   528
Leu Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala
                165   170   175

ttg ttc aag ttc gag gtt tat ttt ggg ctc ttg gtg ttt gtg ggc tat   576
Leu Phe Lys Phe Glu Val Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr
            180   185   190

atc att ttt gac acc caa gat ata att gag aag gca cac ctt ggg gat   624
Ile Ile Phe Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp
            195   200   205

ttg gac tac gtg aag cat gct ctg acc ctc ttt aca gat ttt gtt gct   672
Leu Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
    210   215   220

gtt ttt gtg cga ata tta atc ata atg ctg aag aat gca tcc gac aag   720
Val Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Asp Lys
225   230   235   240

gaa gag aag aag aag aag agg aga aac taatgcataa gcggttattc   767
Glu Glu Lys Lys Lys Lys Arg Arg Asn
            245

aaagactctg taactctaga atctggcatt ttcttgttca taaacttctg tagaccttcg 827

acaagtatgt tgttaatagt ttggtaacgc ctcagattaa gctgcgaggc tctgttatgc 887

cgcatgccaa tgtggttatg gtggtacata gatggttttg tttccgaagc ataccatcaa 947

ataacatgca tgtttacact atatcgataa cctacgagtg tactacttat ttctgctccc 1007

ttttgctgtg ttaggttgtt catgattgta tagttgattt ccgttatgt tagaccatct 1067

tctttcttga cgtttaattt ctcatattga tgggagaaat gaaaattcac accgtcgccc 1127

caacttgttt aagactgagg cgcaattgta gtt   1160

<210> 6
<211> 249
<212> PRT
<213> Nicotiana tabacum

<400> 6
Met Glu Ser Cys Thr Ser Phe Phe Asn Ser Gln Ser Ala Ser Ser Arg
  1   5   10   15

Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro
                20   25   30

Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala
            35   40   45

Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
    50   55   60

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Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
 65                  70              75                  80

Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
                 85              90                  95

Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
            100             105             110

Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
        115             120             125

Ala Val Ala Phe Gly Cys Phe Ser Ala Ala Ala Met Val Ala Arg Arg
    130             135             140

Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
145             150             155             160

Leu Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala
                165             170             175

Leu Phe Lys Phe Glu Val Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr
            180             185             190

Ile Ile Phe Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp
    195             200             205

Leu Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
    210             215             220

Val Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Asp Lys
225             230             235             240

Glu Glu Lys Lys Lys Lys Arg Arg Asn
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<210> 7
<211> 1056
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(747)
<223> coding for BI1-protein

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Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Tyr Gly Ala Ala Ala Ser
 1               5                  10                  15

ggc tgg ggc tac gac tcg ctg aag aac ttc cgc cag atc tcc ccc gcc    96
Gly Trp Gly Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala
            20              25                  30
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```
gtc cag tcc cac ctc aag ctc gtt tac ctg aca cta tgc gtc gcc ctg      144
Val Gln Ser His Leu Lys Leu Val Tyr Leu Thr Leu Cys Val Ala Leu
         35                  40                  45

gct gcg tcg gcg gtg ggc gca tac ctg cac gtc gcc ttg aac atc ggc      192
Ala Ala Ser Ala Val Gly Ala Tyr Leu His Val Ala Leu Asn Ile Gly
     50                  55                  60

ggg atg ttg act atg ctc ggg tgc gtg ggg agc atc gcc tgg ttg ttc      240
Gly Met Leu Thr Met Leu Gly Cys Val Gly Ser Ile Ala Trp Leu Phe
65                   70                  75                  80

tcg gtg cct gtc ttt gag gag agg aag agg ttt ggg att ctc ttg gcc      288
Ser Val Pro Val Phe Glu Glu Arg Lys Arg Phe Gly Ile Leu Leu Ala
                 85                  90                  95

gct gcc ctg ctg gaa ggg gct tca gtt ggg cct ctg atc aag ctt gct      336
Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Leu Ala
             100                 105                 110

gta gac ttt gac tca agc att ctc gta aca gca ttt gtt gga act gcc      384
Val Asp Phe Asp Ser Ser Ile Leu Val Thr Ala Phe Val Gly Thr Ala
             115                 120                 125

att gca ttt ggg tgc ttc act tgc gct gcc atc gtt gcc aag cgt agg      432
Ile Ala Phe Gly Cys Phe Thr Cys Ala Ala Ile Val Ala Lys Arg Arg
     130                 135                 140

gag tac ctc tac ctt ggt ggt ttg ctc tct tct ggc ctc tcc atc ctg      480
Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu
145                  150                 155                 160

ctc tgg ctg cag ttt gcc gca tcc atc ttt ggc cac tcc acc ggc agc      528
Leu Trp Leu Gln Phe Ala Ala Ser Ile Phe Gly His Ser Thr Gly Ser
                 165                 170                 175

ttc atg ttt gag gtt tac ttt ggc ctg ttg atc ttc ctg ggg tac atg      576
Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met
             180                 185                 190

gtg tat gac acg cag gag atc atc gag agg gct cac cac ggt gac atg      624
Val Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met
         195                 200                 205

gac tac atc aag cac gca ctc acc ctc ttc act gac ttc gtg gcc gtc      672
Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val
     210                 215                 220

ctt gtc cgg atc ctc gtc atc atg ctc aag aac gcg tct gac aag tcg      720
Leu Val Arg Ile Leu Val Ile Met Leu Lys Asn Ala Ser Asp Lys Ser
225                  230                 235                 240

gag gag aag aag agg aag aag agg tct tgagagcttc tcttcccgct           767
Glu Glu Lys Lys Arg Lys Lys Arg Ser
                 245

ttgcacataa gaaaaaacca ccgcggctat tgcctctacg tattatgaca gagccgcact   827
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tcaactgggt tttatggtga atacaagttc ttttgcattt tgttgatacg gtgtgaatct 887

tctcaggttt gtcgtcgtag tagctttgca aatactagca tgctacatga cacggatctt 947

tctgtaatgg tggtcgcgtt gatcgaaacg tgaaaacaca tcttcatttg cgactaattt 1007

gtttgccttt tggtgattga tgatgatcct ttccccaaaa aaaaaaaaa          1056
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<210> 8
<211> 249
<212> PRT
<213> Oryza sativa

<400> 8

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Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Tyr Gly Ala Ala Ala Ser
  1               5                  10                  15

Gly Trp Gly Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala
             20                  25                  30

Val Gln Ser His Leu Lys Leu Val Tyr Leu Thr Leu Cys Val Ala Leu
         35                  40                  45

Ala Ala Ser Ala Val Gly Ala Tyr Leu His Val Ala Leu Asn Ile Gly
     50                  55                  60

Gly Met Leu Thr Met Leu Gly Cys Val Gly Ser Ile Ala Trp Leu Phe
 65                  70                  75                  80

Ser Val Pro Val Phe Glu Glu Arg Lys Arg Phe Gly Ile Leu Leu Ala
             85                  90                  95

Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Leu Ala
            100                 105                 110

Val Asp Phe Asp Ser Ser Ile Leu Val Thr Ala Phe Val Gly Thr Ala
            115                 120                 125

Ile Ala Phe Gly Cys Phe Thr Cys Ala Ala Ile Val Ala Lys Arg Arg
            130                 135                 140

Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu
145                 150                 155                 160

Leu Trp Leu Gln Phe Ala Ala Ser Ile Phe Gly His Ser Thr Gly Ser
                165                 170                 175

Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met
                180                 185                 190

Val Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met
            195                 200                 205

Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val
            210                 215                 220
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Leu Val Arg Ile Leu Val Ile Met Leu Lys Asn Ala Ser Asp Lys Ser
225             230             235             240

Glu Glu Lys Lys Arg Lys Lys Arg Ser
                245
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<210> 9
<211> 973
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(741)
<223> coding for BI1-protein

<400> 9
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Met Asp Ser Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
  1               5                  10                  15

tgg agc tat gat tct ctc aaa aac ctc cgt cag att tct ccc tcc gtc    96
Trp Ser Tyr Asp Ser Leu Lys Asn Leu Arg Gln Ile Ser Pro Ser Val
                20                  25                  30

cag aat cat ctc aag agg gtt tat ctc act ctg tgt tgt gct ctc gtt   144
Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
            35                  40                  45

gcg tct gcg ttt gga gct tac ctc cac gtg ctc tgg aac ata ggt ggt   192
Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
        50                  55                  60

att ctc act acc att gga tgc ttt gga agc atg att tgg ctg ctc tcc   240
Ile Leu Thr Thr Ile Gly Cys Phe Gly Ser Met Ile Trp Leu Leu Ser
 65                  70                  75                  80

tgt cct cct tat gaa caa caa aag agg ctt tcc ctt ctg ttt ctg tct   288
Cys Pro Pro Tyr Glu Gln Gln Lys Arg Leu Ser Leu Leu Phe Leu Ser
                85                  90                  95

gct gtt ctc gaa ggt gct tca gtt ggt ccc ttg atc aaa gtg gca gtt   336
Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Val
            100                 105                 110

gat ttt gac cca agc atc ctc atc act gcg ttt gtc gga act gcg ata   384
Asp Phe Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
            115                 120                 125

gcc ttt atc tgt ttc tca ggg gca gcg atg ttg gca aga cgc aga gag   432
Ala Phe Ile Cys Phe Ser Gly Ala Ala Met Leu Ala Arg Arg Arg Glu
        130                 135                 140

tac ctc tac ctc gga gga ctg ctt tca tct ggc ttg tcc atg ctt atg   480
Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
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```
        145                    150                    155                    160

tgg ctt cag ttt gcc tct tcc atc ttt ggt ggc tct gca tcc atc ttt   528
Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
                165                    170                    175

aag ttt gag ctc tac ttt gga ctc ttg atc ttt gtg gga tac atg gtg   576
Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
                180                    185                    190

gtg gac act caa gat att ata gag aag gcc cac ctc ggt gac atg gat   624
Val Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
                195                    200                    205

tac gtg aaa cat tcg ttg acc ctt ttc acc gat ttt gta gct gtg ttt   672
Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
            210                    215                    220

gtt cgt gtt ctc atc att atg ctg aag aac tcg gca gat aaa gaa gat   720
Val Arg Val Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Asp
225                    230                    235                    240

aaa aag aag agg agg agg aac tgagactaaa aagtgagaaa gaaagctaaa      771
Lys Lys Lys Arg Arg Arg Asn
                245

tagagtgggt gttatgtgtg tttcaaaaaa taaaaaagag tgggtgttat aagtacagac 831

atgatagcgt tggtgttttt tacttgtttg gaacagtttt ggtaacaaca cacgttacgt 891

atttgtgtat tcctcttagt gactccagat tgtgaatgga tcagtatctt gaaactgtgt 951

tgaaaattat cagttgggag ct                                          973
```

```
<210> 10
<211> 247
<212> PRT
<213> Brassica napus

<400> 10
Met Asp Ser Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
  1               5                    10                    15

Trp Ser Tyr Asp Ser Leu Lys Asn Leu Arg Gln Ile Ser Pro Ser Val
                20                    25                    30

Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
                35                    40                    45

Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
            50                    55                    60

Ile Leu Thr Thr Ile Gly Cys Phe Gly Ser Met Ile Trp Leu Leu Ser
 65                    70                    75                    80

Cys Pro Pro Tyr Glu Gln Gln Lys Arg Leu Ser Leu Leu Phe Leu Ser
```

```
                    85                      90                      95
Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Val
            100                     105                     110

Asp Phe Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
            115                     120                     125

Ala Phe Ile Cys Phe Ser Gly Ala Ala Met Leu Ala Arg Arg Arg Glu
        130                     135                     140

Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
145                     150                     155                     160

Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
                165                     170                     175

Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
            180                     185                     190

Val Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
            195                     200                     205

Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
    210                     215                     220

Val Arg Val Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Asp
225                     230                     235                     240

Lys Lys Lys Arg Arg Arg Asn
                245
```

<210> 11
<211> 747
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(744)
<223> coding for BI1-protein

<400> 11
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cga ttg caa gca atg gac gcc ttc aat tcc ttc ttc gat tca aga aac   48
Arg Leu Gln Ala Met Asp Ala Phe Asn Ser Phe Phe Asp Ser Arg Asn
 1               5                   10                  15

cga tgg aat tac gat act ctc aaa aac ttc cgt cag att tct ccg gtc   96
Arg Trp Asn Tyr Asp Thr Leu Lys Asn Phe Arg Gln Ile Ser Pro Val
            20                  25                  30

gtg cag aat cac ctg aag cag gtt tat ttt act ctg tgt ttt gcc gtg   144
Val Gln Asn His Leu Lys Gln Val Tyr Phe Thr Leu Cys Phe Ala Val
        35                  40                  45

gtt gct gcg gct gtc ggg gct tac ctt cat gtc ctc ttg aac att ggg   192
```

14

```
Val Ala Ala Ala Val Gly Ala Tyr Leu His Val Leu Leu Asn Ile Gly
    50                  55                  60

ggt ttt ctt act aca gtg gca tgc atg gga agc agc ttt tgg tta ctc    240
Gly Phe Leu Thr Thr Val Ala Cys Met Gly Ser Ser Phe Trp Leu Leu
65                  70                  75                  80

tcc aca cct cct ttt gaa gag agg aag agg gtg act ttg ttg atg gcc    288
Ser Thr Pro Pro Phe Glu Glu Arg Lys Arg Val Thr Leu Leu Met Ala
                    85                  90                  95

gca tca ctg ttt cag ggt tcc tct att gga ccc ttg att gat ttg gct    336
Ala Ser Leu Phe Gln Gly Ser Ser Ile Gly Pro Leu Ile Asp Leu Ala
                100                 105                 110

att cat atc gat cca agc ctt atc ttt agt gca ttt gtg gga aca gcc    384
Ile His Ile Asp Pro Ser Leu Ile Phe Ser Ala Phe Val Gly Thr Ala
                115                 120                 125

ttg gcc ttt gca tgc ttc tca gga gca gct ttg gtt gct agg cgt agg    432
Leu Ala Phe Ala Cys Phe Ser Gly Ala Ala Leu Val Ala Arg Arg Arg
    130                 135                 140

gag tac ctg tac ctt ggt ggc ttg gtt tct tct gga ttg tcc atc ctt    480
Glu Tyr Leu Tyr Leu Gly Gly Leu Val Ser Ser Gly Leu Ser Ile Leu
145                 150                 155                 160

ctc tgg ttg cac ttt gct tct tcc atc ttt gga ggc tca aca gct ctc    528
Leu Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Thr Ala Leu
                165                 170                 175

ttt aag ttt gag ttg tac ttt ggg ctt ttg gtg ttt gta ggt tac att    576
Phe Lys Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile
                180                 185                 190

gta gta gac acc caa gaa ata gtt gag agg gca cac ttg ggc gat ctg    624
Val Val Asp Thr Gln Glu Ile Val Glu Arg Ala His Leu Gly Asp Leu
                195                 200                 205

gac tat gta aag cat gcc ttg acc ttg ttt acc gat ttg gtc gca gtt    672
Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Leu Val Ala Val
    210                 215                 220

ttt gtc cgg att ctt gtt att atg ttg aag aat tcg act gag agg aat    720
Phe Val Arg Ile Leu Val Ile Met Leu Lys Asn Ser Thr Glu Arg Asn
225                 230                 235                 240

gag aag aaa aag aag aga aga gat tga                                747
Glu Lys Lys Lys Lys Arg Arg Asp
                245
```

<210> 12
<211> 248
<212> PRT
<213> Glycine max

<400> 12

```
Arg Leu Gln Ala Met Asp Ala Phe Asn Ser Phe Phe Asp Ser Arg Asn
 1               5                  10                  15

Arg Trp Asn Tyr Asp Thr Leu Lys Asn Phe Arg Gln Ile Ser Pro Val
            20                  25                  30

Val Gln Asn His Leu Lys Gln Val Tyr Phe Thr Leu Cys Phe Ala Val
        35                  40                  45

Val Ala Ala Ala Val Gly Ala Tyr Leu His Val Leu Leu Asn Ile Gly
    50                  55                  60

Gly Phe Leu Thr Thr Val Ala Cys Met Gly Ser Ser Phe Trp Leu Leu
65                  70                  75                  80

Ser Thr Pro Pro Phe Glu Glu Arg Lys Arg Val Thr Leu Leu Met Ala
            85                  90                  95

Ala Ser Leu Phe Gln Gly Ser Ser Ile Gly Pro Leu Ile Asp Leu Ala
        100                 105                 110

Ile His Ile Asp Pro Ser Leu Ile Phe Ser Ala Phe Val Gly Thr Ala
        115                 120                 125

Leu Ala Phe Ala Cys Phe Ser Gly Ala Ala Leu Val Ala Arg Arg Arg
    130                 135                 140

Glu Tyr Leu Tyr Leu Gly Gly Leu Val Ser Ser Gly Leu Ser Ile Leu
145                 150                 155                 160

Leu Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Thr Ala Leu
            165                 170                 175

Phe Lys Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile
            180                 185                 190

Val Val Asp Thr Gln Glu Ile Val Glu Arg Ala His Leu Gly Asp Leu
        195                 200                 205

Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Leu Val Ala Val
    210                 215                 220

Phe Val Arg Ile Leu Val Ile Met Leu Lys Asn Ser Thr Glu Arg Asn
225                 230                 235                 240

Glu Lys Lys Lys Lys Arg Arg Asp
                245
```

<210> 13
<211> 1510
<212> DNA
<213> Glycine max

<220>
<221> misc_feature

<220>
<221> CDS
<222> (1046)..(1095)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (1)..(777)
<223> coding for BI-1 protein

<400> 13
```
atc acg aaa act ata cga ttc gat tcc ttg ttt tcg atg gac act ttc      48
Ile Thr Lys Thr Ile Arg Phe Asp Ser Leu Phe Ser Met Asp Thr Phe
 1               5                  10                  15


ttc aag tcc cca tct tct tct tct tcg aga agc cgc tgg agt tac gat      96
Phe Lys Ser Pro Ser Ser Ser Ser Ser Arg Ser Arg Trp Ser Tyr Asp
                20                  25                  30


act ctc aag aat ttc cgc gag atc tct ccg ctc gtt cag aat cac atc     144
Thr Leu Lys Asn Phe Arg Glu Ile Ser Pro Leu Val Gln Asn His Ile
            35                  40                  45


aaa ctg gtt tat ttt acg tta tgt tgc gct gtg gtg gct gct gct gtt     192
Lys Leu Val Tyr Phe Thr Leu Cys Cys Ala Val Val Ala Ala Ala Val
        50                  55                  60


gga gct ttc ctt cat gtt ctg tgg aac att ggc ggt ttt ctc acc acg     240
Gly Ala Phe Leu His Val Leu Trp Asn Ile Gly Gly Phe Leu Thr Thr
 65                  70                  75                  80


ttg gct tcc att ggg agc atg ttt tgg ttg cta tct aca ccc cct ttt     288
Leu Ala Ser Ile Gly Ser Met Phe Trp Leu Leu Ser Thr Pro Pro Phe
                85                  90                  95


gaa gag caa aag agg ttg tct ctg ttg atg gct tcg gcc ctg ttt cag     336
Glu Glu Gln Lys Arg Leu Ser Leu Leu Met Ala Ser Ala Leu Phe Gln
                100                 105                 110


ggt gct tcc att gga cct ctg att gat ttg gct ttt gcc att gat cct     384
Gly Ala Ser Ile Gly Pro Leu Ile Asp Leu Ala Phe Ala Ile Asp Pro
            115                 120                 125


ggc ctt atc att ggc gca ttt gtg gca act tct ttg gct ttt gct tgc     432
Gly Leu Ile Ile Gly Ala Phe Val Ala Thr Ser Leu Ala Phe Ala Cys
        130                 135                 140


ttt tct gca gta gcc tta gtt gca agg cga agg gag tac ctc tac ctt     480
Phe Ser Ala Val Ala Leu Val Ala Arg Arg Arg Glu Tyr Leu Tyr Leu
145                 150                 155                 160


ggt ggt ttg ctt tct tct tgg ctt tcc att ctt atg tgg ttg cac tct     528
Gly Gly Leu Leu Ser Ser Trp Leu Ser Ile Leu Met Trp Leu His Ser
                165                 170                 175


gat tcc tct ctc ttt ggg ggc tca att gca ctc ttc aag ttt gag ctg     576
Asp Ser Ser Leu Phe Gly Gly Ser Ile Ala Leu Phe Lys Phe Glu Leu
            180                 185                 190
```

```
tac ttt ggg ctt ttg gtg ttt gtg ggc tac gtt ata gta gac act caa    624
Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Val Ile Val Asp Thr Gln
        195                 200                 205

gaa att att gaa agg gct cac ttt ggt gac ctg gat tat gtg aag cat    672
Glu Ile Ile Glu Arg Ala His Phe Gly Asp Leu Asp Tyr Val Lys His
    210                 215                 220

gca ttg aca ttg ttc act gat ttg gct gca atc ttt gtg cga att ctt    720
Ala Leu Thr Leu Phe Thr Asp Leu Ala Ala Ile Phe Val Arg Ile Leu
225                 230                 235                 240

att ata atg ttg aag aat tca tct gag aga aat gag aag aag aag aaa    768
Ile Ile Met Leu Lys Asn Ser Ser Glu Arg Asn Glu Lys Lys Lys Lys
                245                 250                 255

agg aga gat tagtaggctg accgaccgac tcgagctcag gcttctctac           817
Arg Arg Asp

agtaatttag tttgtggaga atacataatt agctgtttag atgatgttgg tcccttgtgt 877

agttagttag ctatgtgttt gctgtaatgg taaatgtcag gatttctttt aaacatcttc 937

atatgtattt gccaatatca taatgtgtcg tataacatca taccttggtt taaaaaaaaa 997

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaann nnnnnnnnnn 1057

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnngg tgtttgtggg ctacgttata 1117

gtagacactc aagtaatcat tgagagggct cactttggtg acctggatta tgttaagcat 1177

gcattgacac tgttcactga tttggctgca atctttgtgc gaattcttaa tataatgttg 1237

aataattcat ctaagagaaa tgagaagaag aggaggagag attaataggt tgaccgattg 1297

ctatgtgtag agtaatttgg tttgtagaga atacataatt agctgtttag aagttgttgg 1357

tccccttgtg tagttagtag ttagctatgt gtttgctgta atggtaaatg tcaggatttc 1417

ttttaaacat tttcatatgt atttgctaat aatcataata tatagtataa acatcattcc 1477

ttggtttaaa aaagaaaaa aaaaaaaaaa aaa                                1510
```

<210> 14
<211> 259
<212> PRT
<213> Glycine max

<400> 14

```
Ile Thr Lys Thr Ile Arg Phe Asp Ser Leu Phe Ser Met Asp Thr Phe
 1               5                   10                  15

Phe Lys Ser Pro Ser Ser Ser Ser Ser Arg Ser Arg Trp Ser Tyr Asp
            20                  25                  30
```

Thr Leu Lys Asn Phe Arg Glu Ile Ser Pro Leu Val Gln Asn His Ile
   35   40   45

Lys Leu Val Tyr Phe Thr Leu Cys Cys Ala Val Val Ala Ala Ala Val
   50   55   60

Gly Ala Phe Leu His Val Leu Trp Asn Ile Gly Gly Phe Leu Thr Thr
65   70   75   80

Leu Ala Ser Ile Gly Ser Met Phe Trp Leu Leu Ser Thr Pro Pro Phe
     85   90   95

Glu Glu Gln Lys Arg Leu Ser Leu Leu Met Ala Ser Ala Leu Phe Gln
    100   105   110

Gly Ala Ser Ile Gly Pro Leu Ile Asp Leu Ala Phe Ala Ile Asp Pro
   115   120   125

Gly Leu Ile Ile Gly Ala Phe Val Ala Thr Ser Leu Ala Phe Ala Cys
  130   135   140

Phe Ser Ala Val Ala Leu Val Ala Arg Arg Arg Glu Tyr Leu Tyr Leu
145   150   155   160

Gly Gly Leu Leu Ser Ser Trp Leu Ser Ile Leu Met Trp Leu His Ser
    165   170   175

Asp Ser Ser Leu Phe Gly Gly Ser Ile Ala Leu Phe Lys Phe Glu Leu
   180   185   190

Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Val Ile Val Asp Thr Gln
  195   200   205

Glu Ile Ile Glu Arg Ala His Phe Gly Asp Leu Asp Tyr Val Lys His
  210   215   220

Ala Leu Thr Leu Phe Thr Asp Leu Ala Ala Ile Phe Val Arg Ile Leu
225   230   235   240

Ile Ile Met Leu Lys Asn Ser Ser Glu Arg Asn Glu Lys Lys Lys Lys
   245   250   255

Arg Arg Asp

<210> 15
<211> 651
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(651)
<223> coding for BI-1 protein

<400> 15

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gtc gca atg ccg ggt cga cga ttt cgt ctg acc tat gct ttg cct ggc    48
Val Ala Met Pro Gly Arg Arg Phe Arg Leu Thr Tyr Ala Leu Pro Gly
 1               5                  10                  15

ctc atc tgc cgt ggg tgc tta cct gca cat tgc cct gaa cat tgg cgg    96
Leu Ile Cys Arg Gly Cys Leu Pro Ala His Cys Pro Glu His Trp Arg
             20                  25                  30

gat gct gac aat gct cgc gtg tat cgg aac cat cgc ctg gat gtt ctc   144
Asp Ala Asp Asn Ala Arg Val Tyr Arg Asn His Arg Leu Asp Val Leu
         35                  40                  45

ggt gcc agt cta cga gga gag gaa gag gtt tgg gct gct gat ggg tgc   192
Gly Ala Ser Leu Arg Gly Glu Glu Glu Val Trp Ala Ala Asp Gly Cys
     50                  55                  60

agc ctc ctg gaa ggg gct tca gtt gga cct ctg att gag ctt gcc ata   240
Ser Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile
 65                  70                  75                  80

gac ttt gac cca agt atc ctc gtg aca ggg ttt gtc gga acc gcc atc   288
Asp Phe Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile
                 85                  90                  95

gcc ttc ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag   336
Ala Phe Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu
             100                 105                 110

tac ctg tac ctc ggt ggt ctg ctc tcc tcc ggc ctg tcg atc ctg ctc   384
Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu
         115                 120                 125

tgg ctg cag ttt gcc acg tcc atc ttt ggc cac tcc tct ggc agc ttc   432
Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe
     130                 135                 140

atg ttt gag gtt tac ttt ggc ctg ttg atc ttc ctg gga tac atg gtg   480
Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val
145                 150                 155                 160

tac gac acg cag gag atc atc gag agg gcg cac cac ggc gac atg gat   528
Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp
                 165                 170                 175

tac atc aag cac gcg ctc acc ctc ttc acc gac ttc gtc gcc gtt ctc   576
Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu
             180                 185                 190

gtc cgc gtc ctc atc atc ttg ctc aag aac gca gcg gac aag gtc gga   624
Val Arg Val Leu Ile Ile Leu Leu Lys Asn Ala Ala Asp Lys Val Gly
         195                 200                 205

ggc caa gaa gag gag gaa gag aag tcc                                651
Gly Gln Glu Glu Glu Glu Glu Lys Ser
         210                 215
```

<210> 16
<211> 217
<212> PRT
<213> Triticum aestivum

<400> 16
Val Ala Met Pro Gly Arg Arg Phe Arg Leu Thr Tyr Ala Leu Pro Gly
1   5   10   15

Leu Ile Cys Arg Gly Cys Leu Pro Ala His Cys Pro Glu His Trp Arg
            20   25   30

Asp Ala Asp Asn Ala Arg Val Tyr Arg Asn His Arg Leu Asp Val Leu
        35   40   45

Gly Ala Ser Leu Arg Gly Glu Glu Glu Val Trp Ala Ala Asp Gly Cys
    50   55   60

Ser Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile
65   70   75   80

Asp Phe Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile
            85   90   95

Ala Phe Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu
            100   105   110

Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu
        115   120   125

Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe
    130   135   140

Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val
145   150   155   160

Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp
            165   170   175

Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu
        180   185   190

Val Arg Val Leu Ile Ile Leu Leu Lys Asn Ala Ala Asp Lys Val Gly
        195   200   205

Gly Gln Glu Glu Glu Glu Glu Lys Ser
    210   215

<210> 17
<211> 412
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(410)

<223> coding for BI1-protein

<400> 17
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tt gtt att gac ttg gat tcg agg att ctc gtc act gcg ttc gtc ggg      47
   Val Ile Asp Leu Asp Ser Arg Ile Leu Val Thr Ala Phe Val Gly
    1               5                  10                  15

acc gca gtt gct ttt gca tgc ttc tct ggc gct gcc atc atc gcc aag      95
Thr Ala Val Ala Phe Ala Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys
                20                  25                  30

cgc agg gaa tac ctg tac ctc ggc ggt ctg ctt tca tct ggc ctc tcc     143
Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser
            35                  40                  45

att ctt ctc tgg ctg cag ttt gct act tca atc ttt ggc cac acc agc     191
Ile Leu Leu Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Thr Ser
        50                  55                  60

gcg acc ttc atg ttt gag ctc tac ttt ggc ctc ctg gtt ttc ctg gga     239
Ala Thr Phe Met Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Leu Gly
    65                  70                  75

tat atg gtg ttt gac acc cag gag atc atc gag agg gcg cac cgt ggg     287
Tyr Met Val Phe Asp Thr Gln Glu Ile Ile Glu Arg Ala His Arg Gly
 80                  85                  90                  95

gac atg gac tac atc aag cac gcg ctg act ctc ttc acc gac ttt gtt     335
Asp Met Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val
                100                 105                 110

gcg gtt ctt gtt cga atc ctt gtc atc atg atg aag aat gca cag gag     383
Ala Val Leu Val Arg Ile Leu Val Ile Met Met Lys Asn Ala Gln Glu
            115                 120                 125

aaa tcc caa gac gag aag aag agg aag aa                              412
Lys Ser Gln Asp Glu Lys Lys Arg Lys
        130                 135
```

<210> 18
<211> 136
<212> PRT
<213> Zea mays

<400> 18
```
Val Ile Asp Leu Asp Ser Arg Ile Leu Val Thr Ala Phe Val Gly Thr
 1               5                  10                  15

Ala Val Ala Phe Ala Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg
                20                  25                  30

Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
            35                  40                  45

Leu Leu Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Thr Ser Ala
        50                  55                  60
```

```
Thr Phe Met Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Leu Gly Tyr
 65              70              75              80

Met Val Phe Asp Thr Gln Glu Ile Ile Glu Arg Ala His Arg Gly Asp
            85              90              95

Met Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
            100             105             110

Val Leu Val Arg Ile Leu Val Ile Met Met Lys Asn Ala Gln Glu Lys
        115             120             125

Ser Gln Asp Glu Lys Lys Arg Lys
    130             135


<210> 19
<211> 345
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(342)

<400> 19
gcc gcc atc atc gcc aag cgc agg gag tac ctg tac ctc ggt ggc ctg      48
Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu
 1               5               10              15

ctc tcc tcc ggc ctg tcg atc ctg ctc tgg ctg cag ttt gcc acg tcc      96
Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Thr Ser
            20              25              30

atc ttt ggc cac tcc tct ggc agc ttc atg ttt gag gtt tac ttt ggc     144
Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe Glu Val Tyr Phe Gly
            35              40              45

ctg ttg atc ttt ctg gga tac atg gtg tac gac acg cag gag atc atc     192
Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Ile Ile
     50              55              60

gag agg gcg cac cac ggc gac atg gac tac atc aag cac gcg ctc acc     240
Glu Arg Ala His His Gly Asp Met Asp Tyr Ile Lys His Ala Leu Thr
 65              70              75              80

ctc ttc acc gac ttt gtc gcc gtc ctc gtc cgg atc ctc atc atc atg     288
Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg Ile Leu Ile Ile Met
            85              90              95

ctc aag aac gca ggc gac aag tcg gag gac aag aag aag agg aag agg     336
Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys Lys Lys Arg Lys Arg
            100             105             110

agg tcc tga                                                          345
Arg Ser
```

<210> 20
<211> 114
<212> PRT
<213> Triticum aestivum

<400> 20

```
Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu
 1               5                  10                  15

Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Thr Ser
                20                  25                  30

Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe Glu Val Tyr Phe Gly
            35                  40                  45

Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Ile Ile
     50                  55                  60

Glu Arg Ala His His Gly Asp Met Asp Tyr Ile Lys His Ala Leu Thr
 65                  70                  75                  80

Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg Ile Leu Ile Ile Met
                85                  90                  95

Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys Lys Lys Arg Lys Arg
            100                 105                 110

Arg Ser
```

<210> 21
<211> 403
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(402)
<223> coding for BI1-protein

<400> 21

```
ggc agc atc gcc tgg ctc ttc tcg gtg ccc gtc tac gag gag agg aag    48
Gly Ser Ile Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys
 1               5                  10                  15

agg tac tgg ctg ctg atg gcg gct gcc ctc ctg gaa ggg gcg tcg gtt    96
Arg Tyr Trp Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val
                20                  25                  30

gga ccc ctc atc aag ctc gcc gtg gaa ttt gac cca agc atc ctg gtg   144
Gly Pro Leu Ile Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val
            35                  40                  45
```

aca gcg ttc gtg ggg act gcc att gcg ttc gcg tgc ttc tct tgc gcg   192
Thr Ala Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Cys Ala
    50   55   60

gcc atg gtg gcc aag cgc agg gag tac ctc tac ctg ggc ggg ctg ctc   240
Ala Met Val Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
65   70   75   80

tct tct ggc ctc tcc atc ctg ctc tgg ctg cag ttc gcc gcc tcc atc   288
Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Ala Ser Ile
                85   90   95

ttc ggc cac caa tcc act agc agc ttc atg ttt gag gtc tac ttt ggg   336
Phe Gly His Gln Ser Thr Ser Ser Phe Met Phe Glu Val Tyr Phe Gly
                100   105   110

ctg ctc atc ttc ctg ggc tac atg gtg tac gac acg cag gag gtc atc   384
Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Val Ile
                115   120   125

gag agg gcg cac cac ggc g   403
Glu Arg Ala His His Gly
    130

<210> 22
<211> 134
<212> PRT
<213> Zea mays

<400> 22
Gly Ser Ile Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys
  1   5   10   15

Arg Tyr Trp Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val
                20   25   30

Gly Pro Leu Ile Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val
            35   40   45

Thr Ala Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Cys Ala
    50   55   60

Ala Met Val Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
65   70   75   80

Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Ala Ser Ile
                85   90   95

Phe Gly His Gln Ser Thr Ser Ser Phe Met Phe Glu Val Tyr Phe Gly
                100   105   110

Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Val Ile
                115   120   125

Glu Arg Ala His His Gly
    130

<210> 23
<211> 410
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(410)
<223> coding for BI1-protein

<400> 23

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gc tgg aac atc ggc gtg agg ctg aca atg ctc ggt tgc atc ggc agc      47
   Trp Asn Ile Gly Val Arg Leu Thr Met Leu Gly Cys Ile Gly Ser
    1               5                  10                  15

atc gac tgg ctc ttc tcg gtg ccc gtc tac gag gag agg aag agg tat     95
Ile Asp Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr
                 20                  25                  30

ggg ctg ctg atg gcg gct gcc ctc ctg gaa ggc gct tcg gtc gga ccc    143
Gly Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro
             35                  40                  45

ctc gtc aag ctc gcc gtg gaa ttt gac cca agc atc ctg gtg acg gcg    191
Leu Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala
         50                  55                  60

ttc gtg ggg act gcc atc gcg ttc gcg tgc ttc tcc ggc gcg gcc atg    239
Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Ala Met
     65                  70                  75

gtg gcc agg cgc agg gag tac ctc tac ctg ggc ggg ctg ctc tcg tcg    287
Val Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser
 80                  85                  90                  95

ggg ctc tcc atc ctg ctc tgg ctg cag ctc gcc gcc tcc atc ttc ggc    335
Gly Leu Ser Ile Leu Leu Trp Leu Gln Leu Ala Ala Ser Ile Phe Gly
                100                 105                 110

cac tcc gca acc agc ttc atg ttc gag gtc tac ttc ggg ctg ctc atc    383
His Ser Ala Thr Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile
            115                 120                 125

ttc ctg ggc tac gtg gtg tac gac acg                                410
Phe Leu Gly Tyr Val Val Tyr Asp Thr
        130                 135
```

<210> 24
<211> 136
<212> PRT
<213> Zea mays

<400> 24

Trp Asn Ile Gly Val Arg Leu Thr Met Leu Gly Cys Ile Gly Ser Ile

```
    1              5                    10                    15

Asp Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr Gly
            20                  25                  30

Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu
        35                  40                  45

Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala Phe
    50                  55                  60

Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Ala Met Val
65                  70                  75                  80

Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly
                85                  90                  95

Leu Ser Ile Leu Leu Trp Leu Gln Leu Ala Ala Ser Ile Phe Gly His
            100                 105                 110

Ser Ala Thr Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe
        115                 120                 125

Leu Gly Tyr Val Val Tyr Asp Thr
        130                 135


<210> 25
<211> 463
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(462)
<223> coding for BI1-protein

<400> 25
ttc tca ggt acg ttc cgc aat tcc cgg agc gac gat ttc gtg ctc tgc    48
Phe Ser Gly Thr Phe Arg Asn Ser Arg Ser Asp Asp Phe Val Leu Cys
  1               5                   10                  15

gaa ctt cag cga gag ctc ccc cga tgc cgg gac gca acc ttg acg gtc    96
Glu Leu Gln Arg Glu Leu Pro Arg Cys Arg Asp Ala Thr Leu Thr Val
            20                  25                  30

gta tac gtg atc cca ata gtg ggc cga ata aaa tct gcc gcg ggt gct   144
Val Tyr Val Ile Pro Ile Val Gly Arg Ile Lys Ser Ala Ala Gly Ala
            35                  40                  45

tac ctg cac att gcc ctg aac atc ggt ggg atg ctg aca atg ctt gcg   192
Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu Thr Met Leu Ala
        50                  55                  60

tgt atc gga acc att gcc tgg atg ttc tct gtg cca gtc tat gag gag   240
Cys Ile Gly Thr Ile Ala Trp Met Phe Ser Val Pro Val Tyr Glu Glu
65                  70                  75                  80
```

```
agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc ctg gaa ggg gct    288
Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu Leu Glu Gly Ala
                85                  90                  95

tcg gtt gga cct ctg att gag ctt gcc ata gac ttt gac cca agc atc    336
Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe Asp Pro Ser Ile
                100                 105                 110

ctc gtg aca ggg ttt gtt gga acc gcc atc gcc ttt ggg tgc ttc tct    384
Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe Gly Cys Phe Ser
                115                 120                 125

ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg tac ctc gga ggc    432
Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly
    130                 135                 140

ctg ctc tcc tcc ggc ctg acg atc ctg ctc t                          463
Leu Leu Ser Ser Gly Leu Thr Ile Leu Leu
145                 150
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<210> 26
<211> 154
<212> PRT
<213> Triticum aestivum

<400> 26

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Phe Ser Gly Thr Phe Arg Asn Ser Arg Ser Asp Asp Phe Val Leu Cys
  1               5                   10                  15

Glu Leu Gln Arg Glu Leu Pro Arg Cys Arg Asp Ala Thr Leu Thr Val
                20                  25                  30

Val Tyr Val Ile Pro Ile Val Gly Arg Ile Lys Ser Ala Ala Gly Ala
            35                  40                  45

Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu Thr Met Leu Ala
    50                  55                  60

Cys Ile Gly Thr Ile Ala Trp Met Phe Ser Val Pro Val Tyr Glu Glu
 65                 70                  75                  80

Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu Leu Glu Gly Ala
                85                  90                  95

Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe Asp Pro Ser Ile
                100                 105                 110

Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe Gly Cys Phe Ser
                115                 120                 125

Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly
    130                 135                 140

Leu Leu Ser Ser Gly Leu Thr Ile Leu Leu
145                 150
```

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<210> 27
<211> 388
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(386)
<223> coding for BI1-protein

<400> 27
tc tgg aac atc ggc ggg acg ctg aca atg ctc ggt tgc gtc ggc agc      47
   Trp Asn Ile Gly Gly Thr Leu Thr Met Leu Gly Cys Val Gly Ser
     1            5                  10                  15

atc gcc tgg ctc ttc tcg gtg ccc gtc tac gag gag agg aag agg tat     95
Ile Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr
              20                  25                  30

ggg ctg ctg atg gcg gct gcc ctc ctg gaa ggc gct tcg gtc gga ccc    143
Gly Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro
              35                  40                  45

ctc gtc aag ctc gcc gtg gaa ttt gac cca agc atc ctg gtg acg gcg    191
Leu Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala
          50                  55                  60

ttc gtg ggg act gcc atc gcg ttc gcg tgc ttc tcc ggc gcg cca tgg    239
Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Pro Trp
      65                  70                  75

tgg cag gcc agg gag tac ctc tac ctg ggc ggc tgc tct cgt cga ggc    287
Trp Gln Ala Arg Glu Tyr Leu Tyr Leu Gly Gly Cys Ser Arg Arg Gly
  80                  85                  90                  95

tct cca tcc tgc tct ggc tgc agc tcg ccg cct cca tct tcg gca ctc    335
Ser Pro Ser Cys Ser Gly Cys Ser Ser Pro Pro Ser Ser Ala Leu
                  100                 105                 110

cgc aac agc ttc atg ttc gag gtc tac ttc ggg ctg ctc att ctt ctg    383
Arg Asn Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Leu Leu
              115                 120                 125

ggc ta                                                             388
Gly


<210> 28
<211> 128
<212> PRT
<213> Zea mays

<400> 28
Trp Asn Ile Gly Gly Thr Leu Thr Met Leu Gly Cys Val Gly Ser Ile
  1            5                  10                  15
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Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr Gly
        20   25   30

Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu
        35   40   45

Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala Phe
    50   55   60

Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Pro Trp Trp
65   70   75   80

Gln Ala Arg Glu Tyr Leu Tyr Leu Gly Gly Cys Ser Arg Arg Gly Ser
            85   90   95

Pro Ser Cys Ser Gly Cys Ser Ser Pro Pro Pro Ser Ser Ala Leu Arg
            100   105   110

Asn Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Leu Leu Gly
        115   120   125

<210> 29
<211> 1737
<212> DNA
<213> Solanum tuberosum

<220>
<221> promoter
<222> (1)..(1737)
<223> patatin promoter

<400> 29
aagcttatgt tgccatatag agtagtttgt gatggtatac ttcataaact ttaacttatg 60
ttaaatttgt aatgataaaa ttttttattgt aaattaaaaa ttacttataa aattgggcat 120
tataacatat gaaagacaaa ttgtgttaca tattttactt ttgactttaa tatgaatatt 180
tcaatttaaa tcattgtttt attttctctt tctttttaca ggtataaaag gtgaaaattg 240
aagcaagatt gattgcaagc tatgtgtcac cacgttattg atactttgga agaaattttt 300
acttatatgt ctttgtttag gagtaatatt tgatatgttt tagttagatt ttcttgtcat 360
ttatgctttta gtataatttt agttatttt attatatgat catgggtgaa ttttgataca 420
aatattttg tcattaaata aattaattta tcacaacttg attacttca gtgacaaaaa 480
atgtattgtc gtagtaccct tttttgttga atatgaataa tttttttttat tttgtgacaa 540
ttgtaattgt cactacttat gataatattt agtgacatat atgtcgtcgg taaaagcaaa 600
cactttcagt gacaaaataa tagatttaat cacaaaatta ttaacctttt ttataataat 660
aaatttatcc ctaatttata catttaagga caaagtattt ttttatata taaaaaatag 720
tctttagtga cgatcgtagt gttgagtcta gaaatcataa tgttgaatct agaaaaatct 780
catgcagtgt aaaataaacc tcaaaaagga cgttcagtcc atagaggggg tgtatgtgac 840
accccaacct cagcaaaaga aaacctccct tcaacaagga catttgcggt gctaaacaat 900
ttcaagtctc atcacacata tatttattat ataatactaa taaagaatag aaaaggaaag 960
gtaaacatca ttaaatcgtc tttgtatatt tttagtgaca actgattgac gaaatctttt 1020
tcgtcacaca aaattttag tgacgaaaca tgatttatag atgatgaaat tatttgtccc 1080
tcataatcta atttgttgta gtgatcatta ctcctttgtt tgtttttattt gtcatgttag 1140
tccattaaaa aaaaatatct ctcttcttat gtacgtgaat ggttggaacg gatctattat 1200
ataatactaa taaagaatag aaaaaggaaa gtgagtgagg ttcgagggag agaatctgtt 1260
taatatcaga gtcgatcatg tgtcaatttt atcgatatga ccctaacttc aactgagttt 1320
aaccaattcc gataaggcga gaaatatcat agtattgagt ctagaaaaat ctcatgtagt 1380

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gtggggtaaa cctcagcaag gacgttgagt ccatagaggg gggtgtatgt gacaccccaa 1440
cctcagcaaa agaaaacctc ccctcaagaa ggacatttgc ggtgctaaac aatttcaagt 1500
ctcatcacac atatatatat attatataat actaataaat aatagaaaaa ggaaaggtaa 1560
acatcactaa cgacagttgc ggtgcaaact gagtgaggta ataaacatca ctaactttta 1620
ttggttatgt caaactcaaa gtaaaatttc tcaacttgtt tacgtgccta tatataccat 1680
gcttgttata tgctcaaagc accaacaaaa tttaaaaaca ctttgaacat ttgcaaa 1737
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<210> 30
<211> 1317
<212> DNA
<213> Triticum aestivum

<220>
<221> promoter
<222> (1)..(1317)
<223> germin 9f-3.8 gene promoter

<400> 30
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tgtcgtgagt tccaagttgc tgaaacttga gaagatccat accgacgaca atggttcaga 120
tatgatgacc aagatattgc gaaataagaa gctacaagca tgttgcaagg tagcgggcat 180
ggcggtgccc ccatcatgag tcggagggg agatttgttg ggatatcctc ctcatgtggg 240
ttctgaggag atgaccattt gaggcctttt agccagccca aagaggtgca gaagcccact 300
acccattagg gttatgacct agggtcattt tggactttgc acatgagtgg atggggatgc 360
tttaccctcc atccagcagc caccaccaag ggtgacgaaa atcagttcat cctccaagag 420
agaagaagag agaaaaccaa gagagcaagg gaagaagagg aagattgaag gaagaagaaa 480
agggagctcc tccccaaggt tgtgatggtc catatccact atcttgtctc cttcaaactt 540
cggttccacc atctttggta agattgttct aatccctagt tcttgagccc caaatcttgt 600
tgtgttcatc caagattcag aaatcttgat gtatgagatc ctctagtgct gtctagagaa 660
gaatttgttg tatcccacat ttgataatag tggaagagga tttgggtggc ttcggcccat 720
ggttttttccc ctcaagttga ggggttttcc acgtaaaatc tggtgtctct ttgttgatgc 780
ttggtgttgt ccagaaactt actcctacca caagcacta ggggccagtt cttttgggaa 840
attctcccag aattgaccct ctccccagct tctcccagaa ttgtcactcc attttttcttt 900
acaattccta gctagttaag gtctaattag ttaggaattg taaaaaaata tcaagtggca 960
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tatgtttcct tccgtgctaa gcaacgatcc ttgagttagt acatgatgtg gtgctgagat 1140
tactttgttt tcgctgcagt tatcagttaa ccacaagtgc atttgcgtgc taattcccaa 1200
caatatgcca cccgcaactc atccaccata gctcagcagc aaccaccaat gccatagaca 1260
ctctcggtaa acaacctgta gcttatcagt ctagctaagc gtgctgcata gcaagca 1317
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<210> 31
<211> 959
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> promoter
<222> (1)..(959)
<223> CAB-2 promoter

<400> 31
gaattcatgt gtgagggcaa ttagtgattg taaaaataaa attgtgtttt gtaaaaaact 60
tttactgtcg aaattatta gggtgatgaa aaaatcagta aactacgaat gatagcttaa 120
agagtttcta tcaaagtgat tgaggaatag tttgttgcaa attaaacctc taacaaaatg 180
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```
ttttctgttg tggtttttca tctctacaaa ttttgaattt tatgatgaat tagaaagata 240
gaatgagtta ctttagattt taaaaggttg ttcaagttta caaaacagat tactagaatc 300
atgattaaaa atttacaagc tacatattgt ctaaaccaat gatgttgaac ataccagatg 360
atagtttttc agtgtttgaa caatcaattg datagttttt atgtttctgc aaaatatgca 420
aataatcagt gttttttgagt ctttgcattt tgatttaaaa gcaaaaacaa ctgagtttca 480
aggttaaatt aattacatta ttcatgagat ttatcaggtt agtggataaa ctgacaatgg 540
aatcaatgtt attgtaaatt ggtagtgatg ttggacttct aatgttactc tctatgatgt 600
ttcggtcatc ggtatcacac tatctttact tttatttaaa ggaaagatca cacaaataag 660
ttatctctat tcagaactat taagctgctt ccaaaagact tgcaacatgt ggtctcgaaa 720
tgctttggct gcaatgaaaa aatcatagca aaagctagtg gactagagac tgccacataa 780
gaatagtaaa cgttaaaacc aaaatctcaa aaatccaatg agtaaagaga tatagattac 840
ttcatagata acaaacgtta ctcgcaattt tcctatataa tccaacccta cctaaccatt 900
ttcaatcact ctcactcaca agttagtcac caaaaaaaaa aaaaacacaa aaagtttca 959
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<210> 32
<211> 445
<212> DNA
<213> Zea mays

<220>
<221> promoter
<222> (1)..(445)
<223> PPCZm1 promoter

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gaattccaaa aatagacacg gcaattttct tattcacaga aaaaatataa ctacaactaa 60
tccccaagtc cacagggatt agggatcaat ctgcaaaact aaaagtactt ttacagttgt 120
acttggcatg agtcatgtga ccatgagaga ggcgcacggt tcagcaaagc aacataaaat 180
tctccaaacg ggccccgcca cacacgatca ccatcacccc cgggctcccg acccagtaca 240
aatagacacg cacactccca actccccacc catctccgcc gcgcacaccg cccaatcagc 300
caatctcctc ctcctcctcc gctctcagac gagcagcggt tgccatcact ctccacttcc 360
cacgcccgct gcgggctcgc aggcggcaga gaattgtctg tgccgccggg tgggaatttg 420
attcggtcgg attccgtgcg ccgcg                                    445
```

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<210> 33
<211> 5455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
      recombinant expression vector pUbiBI-1

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ccaggacaag cgaggaacct tgcgtgcgag gcgaggccgc cccgctccga ttcgattcga 120
cgcgcaggcg caggcgcagg gatggacgcc ttctactcga cctcgtcggc ggcggcgagc 180
ggctggggcc acgactccct caagaacttc cgccagatct cccccgccgt gcagtcccac 240
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ctacacattg ccctgaacat cggcgggatg ctgacaatgc tcgcttgtgt cggaactatc 360
gcctggatgt tctcggtgcc agtctatgag gagaggaaga ggtttgggct gctgatgggt 420
gcagccctcc tggaaggggc ttcggttgga cctctgattg agcttgccat agactttgac 480
ccaagcatcc tcgtgacagg gtttgtcgga accgccatcg cctttgggtg cttctctggc 540
gccgccatca tcgccaagcg cagggagtac ctgtacctcg gtggcctgct ctcgtctggc 600
ctgtcgatcc tgctctggct gcagtttgtc acgtccatct ttggccactc ctctggcagc 660
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ttcatgtttg aggtttactt tggcctgttg atcttcctgg ggtacatggt gtacgacacg 720
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ctcttcaccg actttgttgc cgtcctcgtc cgagtcctca tcatcatgct caagaacgca 840
ggcgacaagt cggaggacaa gaagaagagg aagagggggt cctgaacgtw tctcccgcac 900
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atacattcaa atatgtatcc gctcatgaga caataaccct gataaatgct tcaataatat 1740
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gcattttgcc ttcctgtttt tgctcaccca gaaacgctgg tgaaagtaaa agatgctgaa 1860
gatcagttgg gtgcacgagt gggttacatc gaactggatc tcaacagcgg taagatcctt 1920
gagagttttc gccccgaaga cgttttcca atgatgagca ctttaaagt tctgctatgt 1980
ggcgcggtat tatcccgtat tgacgccggg caagagcaac tcggtcgccg catacactat 2040
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acagtaagag aattatgcag tgctgccata accatgagtg ataacactgc ggccaactta 2160
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cgtgacacca cgatgcctgt agcaatggca caacgttgc gcaaactatt aactggcgaa 2340
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<212> DNA
<213> Artificial sequence

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<212> DNA
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<210> 37
<211> 744
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(741)
<223> coding for TaBI-1

<400> 37

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atg gac gcc ttc tac tcg acc tcg tcg gcg gcg gcg agc ggc tgg ggc      48
Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
 1               5                   10                  15


tac gac tcc ctc aag aac ttc cgc gag atc tcc ccc gcc gtg cag tcc      96
Tyr Asp Ser Leu Lys Asn Phe Arg Glu Ile Ser Pro Ala Val Gln Ser
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```
                    20                        25                        30

cac ctc aag ctc gtt tac ctg acc cta tgc ttt gcc ctg gcc tca tct    144
His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
          35                    40                    45

gcc gtg ggt gct tac ctg cac att gcc ctg aac atc ggt ggg atg ctg    192
Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
          50                    55                    60

aca atg ctc gcg tgt gtt gga acc atc gcc tgg atg ttc tct gtg cca    240
Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
 65                    70                    75                    80

gtc tat gag gag agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc    288
Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
                85                    90                    95

ctg gaa ggg gct tcg gtt gga cct ctg att gag ctt gcc ata gac ttt    336
Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
               100                   105                   110

gac cca agt atc ctc gtg aca ggg ttt gtc gga acc gcc atc gcc ttc    384
Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
               115                   120                   125

ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg    432
Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
          130                   135                   140

tac ctc ggt ggt ctg ctc tcc tcc ggc ctg tcg atc ctg ctc tgg ctg    480
Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
145                   150                   155                   160

cag ttt gcc acg tcc atc ttt ggc cac tcc tct ggc agc ttc atg ttt    528
Gln Phe Ala Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
               165                   170                   175

gag gtt tac ttt ggc ctg ttg atc ttc ctg gga tac atg gtg tac gac    576
Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
               180                   185                   190

acg cag gag atc atc gag agg gcg cac cac ggc gac atg gat tac atc    624
Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
               195                   200                   205

aag cac gcg ctc acc ctc ttc acc gac ttc gtc gcc gtt ctc gtc cgc    672
Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
          210                   215                   220

gtc ctc atc atc atg ctc aag aac gca ggc gac aag tcg gag gac aag    720
Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
225                   230                   235                   240

aag aag agg aag agg ggg tcc tga                                     744
Lys Lys Arg Lys Arg Gly Ser
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<210> 38
<211> 247
<212> PRT
<213> Triticum aestivum

<400> 38
Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
 1               5                  10                  15

Tyr Asp Ser Leu Lys Asn Phe Arg Glu Ile Ser Pro Ala Val Gln Ser
                20                  25                  30

His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
            35                  40                  45

Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
        50                  55                  60

Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
 65                  70                  75                  80

Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
                85                  90                  95

Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
                100                 105                 110

Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
            115                 120                 125

Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
    130                 135                 140

Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
145                 150                 155                 160

Gln Phe Ala Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
                165                 170                 175

Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
            180                 185                 190

Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
            195                 200                 205

Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
    210                 215                 220

Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
225                 230                 235                 240

Lys Lys Arg Lys Arg Gly Ser
            245
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<210> 39
<211> 1293
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (173)..(1126)
<223> coding for Hordeum vulgare subsp. vulgare syntaxin
      (Ror2)

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caacagctcc acccatcgag gagaatcaag aaaccgcgcc ggcgtggtga tcaaggacat 120

ccatcgatcg atcgaccgac cctgccttgc ctgagtcaac ccggcggcag cc atg aac 178
                                                            Met Asn
                                                             1

aac ctc ttc tcg agc tcg tgg aag cgg gcg ggc gcg ggg ggc gac ggg   226
Asn Leu Phe Ser Ser Ser Trp Lys Arg Ala Gly Ala Gly Gly Asp Gly
            5   10   15

gac ctg gag tcg ggc ggc ggc ggc gtg gag atg acg gcg ccg ccg ggc   274
Asp Leu Glu Ser Gly Gly Gly Gly Val Glu Met Thr Ala Pro Pro Gly
        20   25   30

gcc gcg gcg ggg gcg agc ctg gac cgc ttc ttc gag gac gtg gag tcg   322
Ala Ala Ala Gly Ala Ser Leu Asp Arg Phe Phe Glu Asp Val Glu Ser
    35   40   45   50

atc aag gac gac ctg cgg gag ctg gag cgg atc cag cgc tcc ctc cac   370
Ile Lys Asp Asp Leu Arg Glu Leu Glu Arg Ile Gln Arg Ser Leu His
                55   60   65

gac ggc aac gag tcg ggc aag tcg ctc cac gac gcg tcg gcg gtg cgc   418
Asp Gly Asn Glu Ser Gly Lys Ser Leu His Asp Ala Ser Ala Val Arg
                70   75   80

gcg ctc cgc tcc cgc atg gac gcc gac gtg gcc gcc gcc atc aag aag   466
Ala Leu Arg Ser Arg Met Asp Ala Asp Val Ala Ala Ala Ile Lys Lys
            85   90   95

gcc aag gtg gtg aag ttg cgg ctc gag tcg ctc gac cgc gcc aac gcc   514
Ala Lys Val Val Lys Leu Arg Leu Glu Ser Leu Asp Arg Ala Asn Ala
    100   105   110

gcc aac cgg tcc gtg gcc ggg tgc ggg ccg ggg tcg tcc acg gac cgc   562
Ala Asn Arg Ser Val Ala Gly Cys Gly Pro Gly Ser Ser Thr Asp Arg
115   120   125   130

acc cgc acc tcc gtc gtg gcc ggg ctg cgc aag aag ctg cgg gat gcc   610
Thr Arg Thr Ser Val Val Ala Gly Leu Arg Lys Lys Leu Arg Asp Ala
                135   140   145

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atg gag tcc ttc tcc tcc ctc cgc tcc cgc atc acc tcc gag tac cgg    658
Met Glu Ser Phe Ser Ser Leu Arg Ser Arg Ile Thr Ser Glu Tyr Arg
            150                 155                 160

gaa acc gtg gcc cgc cgc tac ttc acg gtg acg ggg tcc cag ccc gac    706
Glu Thr Val Ala Arg Arg Tyr Phe Thr Val Thr Gly Ser Gln Pro Asp
            165                 170                 175

gag gcc acg ctg gac acg ctg gcg gag acg ggg gag ggg gag cgg ctc    754
Glu Ala Thr Leu Asp Thr Leu Ala Glu Thr Gly Glu Gly Glu Arg Leu
            180                 185                 190

ctg cag cgc gcc atc gcg gag cag cag ggg aga ggg gag gtg ctg ggc    802
Leu Gln Arg Ala Ile Ala Glu Gln Gln Gly Arg Gly Glu Val Leu Gly
195                     200                 205                 210

gtg gtg gcg gag atc cag gag cgg cac ggc gcc gtg gcg gac ctg gag    850
Val Val Ala Glu Ile Gln Glu Arg His Gly Ala Val Ala Asp Leu Glu
                215                 220                 225

cgg tcc ctg ctg gag ctg cag cag gtg ttc aac gac atg gcc gtg ctg    898
Arg Ser Leu Leu Glu Leu Gln Gln Val Phe Asn Asp Met Ala Val Leu
            230                 235                 240

gtg gcg gcg cag ggg gag cag ctg gac gac atc gag ggc cac gtc ggg    946
Val Ala Ala Gln Gly Glu Gln Leu Asp Asp Ile Glu Gly His Val Gly
            245                 250                 255

cgg gcg agg tcg ttc gtc gac cgc ggg cgc gag cag ctg cag gtg gca    994
Arg Ala Arg Ser Phe Val Asp Arg Gly Arg Glu Gln Leu Gln Val Ala
            260                 265                 270

cgc aag cac cag aag agc tcc cgc aag tgg acc ttc atc ggc atc ggc   1042
Arg Lys His Gln Lys Ser Ser Arg Lys Trp Thr Phe Ile Gly Ile Gly
275                     280                 285                 290

atc ctg ctc gtc gtc atc ctc atc atc gtc atc ccc atc gtg ctc aag   1090
Ile Leu Leu Val Val Ile Leu Ile Ile Val Ile Pro Ile Val Leu Lys
                295                 300                 305

aac acc aac aag agc aac aac aac aac agc cag cag tagtggtagg        1136
Asn Thr Asn Lys Ser Asn Asn Asn Asn Ser Gln Gln
            310                 315

aacagcctgt ggatctgttg tctgtctctg atgatcctgg tcctggattg cttcctggtt 1196

gttgttgttg attgtctttt gtggaatttt ttgcgattgt aattactcca tccatgtggt 1256

tcgttgagcc actcgattat tatttcatga ctatata                          1293


<210> 40
<211> 318
<212> PRT
<213> Hordeum vulgare

<400> 40
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Met Asn Asn Leu Phe Ser Ser Ser Trp Lys Arg Ala Gly Ala Gly Gly
1   5   10   15

Asp Gly Asp Leu Glu Ser Gly Gly Gly Val Glu Met Thr Ala Pro
            20   25   30

Pro Gly Ala Ala Ala Gly Ala Ser Leu Asp Arg Phe Phe Glu Asp Val
        35   40   45

Glu Ser Ile Lys Asp Asp Leu Arg Glu Leu Glu Arg Ile Gln Arg Ser
    50   55   60

Leu His Asp Gly Asn Glu Ser Gly Lys Ser Leu His Asp Ala Ser Ala
65   70   75   80

Val Arg Ala Leu Arg Ser Arg Met Asp Ala Asp Val Ala Ala Ala Ile
            85   90   95

Lys Lys Ala Lys Val Val Lys Leu Arg Leu Glu Ser Leu Asp Arg Ala
        100   105   110

Asn Ala Ala Asn Arg Ser Val Ala Gly Cys Gly Pro Gly Ser Ser Thr
        115   120   125

Asp Arg Thr Arg Thr Ser Val Val Ala Gly Leu Arg Lys Lys Leu Arg
        130   135   140

Asp Ala Met Glu Ser Phe Ser Ser Leu Arg Ser Arg Ile Thr Ser Glu
145   150   155   160

Tyr Arg Glu Thr Val Ala Arg Arg Tyr Phe Thr Val Thr Gly Ser Gln
            165   170   175

Pro Asp Glu Ala Thr Leu Asp Thr Leu Ala Glu Thr Gly Glu Gly Glu
        180   185   190

Arg Leu Leu Gln Arg Ala Ile Ala Glu Gln Gln Gly Arg Gly Glu Val
        195   200   205

Leu Gly Val Val Ala Glu Ile Gln Glu Arg His Gly Ala Val Ala Asp
    210   215   220

Leu Glu Arg Ser Leu Leu Glu Leu Gln Gln Val Phe Asn Asp Met Ala
225   230   235   240

Val Leu Val Ala Ala Gln Gly Glu Gln Leu Asp Asp Ile Glu Gly His
            245   250   255

Val Gly Arg Ala Arg Ser Phe Val Asp Arg Gly Arg Glu Gln Leu Gln
            260   265   270

Val Ala Arg Lys His Gln Lys Ser Ser Arg Lys Trp Thr Phe Ile Gly
        275   280   285

Ile Gly Ile Leu Leu Val Val Ile Leu Ile Ile Val Ile Pro Ile Val
    290   295   300

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Leu Lys Asn Thr Asn Lys Ser Asn Asn Asn Asn Ser Gln Gln
305             310             315
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<210> 41
<211> 948
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(945)
<223> coding for Arabidopsis thaliana syntaxin 121
      (SYP121) / syntaxin-related protein (SYR1)
      (At3g11820)

<400> 41

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atg gcg aat ccc gcg gga tca acc ggt ggt gtg aac ctc gac aag ttc     48
Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe
  1               5                  10                  15

ttc gaa gat gtt gaa tct gtg aaa gaa gag cta aag gag cta gat cgg     96
Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg
             20                  25                  30

ctc aac gaa aca ctc tct tca tgt cac gag cag agc aag acg ctt cac    144
Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His
         35                  40                  45

aat gct aaa gcc gtt aaa gat ctc cgg tct aaa atg gac ggt gac gtt    192
Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val
     50                  55                  60

gga gtc gcg ttg aag aag gcg aag atg att aaa gtt aaa ctc gag gcg    240
Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala
 65                  70                  75                  80

cta gat cgt gcc aat gct gct aat cgg agt ctc cct ggc tgt gga cct    288
Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro
                 85                  90                  95

ggt tct tcc tcc gat cga acc agg acc tct gtc ctc aat ggt ctc agg    336
Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg
            100                 105                 110

aag aaa ttg atg gac tct atg gat agt ttc aac cga ttg agg gag ctt    384
Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu
        115                 120                 125

atc tcg tcc gag tat aga gaa act gta cag agg agg tac ttc acc gtc    432
Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val
    130                 135                 140

acc ggc gag aat ccg gat gaa cga acc cta gat cga ctg att tcc act    480
Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr
145                 150                 155                 160
```

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gga gag agt gag aga ttc ttg cag aaa gca ata caa gaa caa gga aga      528
Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg
            165                 170                 175

gga agg gtg tta gac acc att aac gag att caa gaa agg cat gat gcg      576
Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Ala
            180                 185                 190

gtt aaa gac att gag aag aat ctc agg gag ctt cac cag gtg ttt cta      624
Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu
            195                 200                 205

gac atg gcc gtg ctg gta gag cac cag gga gct cag ctt gat gac atc      672
Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile
    210                 215                 220

gag agt cat gtg ggt cga gct agc tcc ttt atc aga ggc gga act gac      720
Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp
225                 230                 235                 240

cag cta caa acc gct cgg gtt tac cag aag aac acg cga aaa tgg aca      768
Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr
                245                 250                 255

tgt att gcc att att att ctc atc atc atc ata act gtt gtg gtt ctt      816
Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Ile Thr Val Val Val Leu
            260                 265                 270

gct gtt tta aaa ccg tgg aac aac agc agt ggc ggc ggc ggc ggt ggt      864
Ala Val Leu Lys Pro Trp Asn Asn Ser Ser Gly Gly Gly Gly Gly Gly
            275                 280                 285

ggt ggt ggg ggt acc act gga gga agt caa cca aat tca ggg aca cca      912
Gly Gly Gly Gly Thr Thr Gly Gly Ser Gln Pro Asn Ser Gly Thr Pro
    290                 295                 300

cca aat cct cct cag gca agg cgt cta ttg cgt tga                      948
Pro Asn Pro Pro Gln Ala Arg Arg Leu Leu Arg
305                 310                 315


<210> 42
<211> 315
<212> PRT
<213> Arabidopsis thaliana

<400> 42
Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe
  1               5                  10                  15

Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg
                20                  25                  30

Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His
            35                  40                  45
```

Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val
  50   55   60

Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala
 65   70   75   80

Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro
      85   90   95

Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg
      100   105   110

Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu
    115   120   125

Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val
  130   135   140

Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr
145   150   155   160

Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg
      165   170   175

Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Ala
     180   185   190

Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu
   195   200   205

Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile
  210   215   220

Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp
225   230   235   240

Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr
     245   250   255

Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Thr Val Val Val Leu
    260   265   270

Ala Val Leu Lys Pro Trp Asn Asn Ser Ser Gly Gly Gly Gly Gly Gly
   275   280   285

Gly Gly Gly Gly Thr Thr Gly Gly Ser Gln Pro Asn Ser Gly Thr Pro
  290   295   300

Pro Asn Pro Pro Gln Ala Arg Arg Leu Leu Arg
305   310   315

<210> 43
<211> 1275
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (80)..(1006)
<223> coding for Hordeum vulgare subsp. vulgare SNAP-34

<400> 43
ggcccctcca ccccaccccca cccagtcgct gcggatactt gattctgcta ctcggccagc 60

gatcgatctc gcctccgcc atg agc gcc acc agg ccc tcc ttc ttc ccc tcc   112
                        Met Ser Ala Thr Arg Pro Ser Phe Phe Pro Ser
                         1   5   10

aac aac aac agg aac aag ccc gcc acc cgg aac ccc ttc gac tcc gac   160
Asn Asn Asn Arg Asn Lys Pro Ala Thr Arg Asn Pro Phe Asp Ser Asp
             15   20   25

tcg gac gac gac ggc ggc atg gcc cgg cgc ggc ccg gcg cgg gcc tcg   208
Ser Asp Asp Asp Gly Gly Met Ala Arg Arg Gly Pro Ala Arg Ala Ser
         30   35   40

tcc gtc ccg acc ccc gcc gcg ggg ccg gcc agg gcc tcc tcg gcc ccg   256
Ser Val Pro Thr Pro Ala Ala Gly Pro Ala Arg Ala Ser Ser Ala Pro
     45   50   55

atc ccc gcc gac gag gcg gac cag cgg ggc gcc ctg ttc ggc gcg ggc   304
Ile Pro Ala Asp Glu Ala Asp Gln Arg Gly Ala Leu Phe Gly Ala Gly
 60   65   70   75

ccc gcg ccg tcc ggc ttc gcg tcc tcc tcc tcc gcg gcc gcc agg ggc   352
Pro Ala Pro Ser Gly Phe Ala Ser Ser Ser Ser Ala Ala Ala Arg Gly
                 80   85   90

cgg tac agg aac gac ttc cgc gac tcg ggc ggc gtg gag gcg cag tcc   400
Arg Tyr Arg Asn Asp Phe Arg Asp Ser Gly Gly Val Glu Ala Gln Ser
                 95   100   105

gtg cag gag ctc gag ggc tac gcg gcc tac aag gcc gag gag acc acg   448
Val Gln Glu Leu Glu Gly Tyr Ala Ala Tyr Lys Ala Glu Glu Thr Thr
             110   115   120

cgc cgg gtc gac ggc tgc ctc cgg gtc gcc gag gag atg cgg gac acc   496
Arg Arg Val Asp Gly Cys Leu Arg Val Ala Glu Glu Met Arg Asp Thr
             125   130   135

gcg tca aag acc ctg ctc cag gtg cac cag cag ggc cag cag atc agg   544
Ala Ser Lys Thr Leu Leu Gln Val His Gln Gln Gly Gln Gln Ile Arg
140   145   150   155

cgc acc cac gcc atg gcc gtc gac atc gac cag gat ctc tcc agg ggg   592
Arg Thr His Ala Met Ala Val Asp Ile Asp Gln Asp Leu Ser Arg Gly
                 160   165   170

gaa aag cta cta ggt gat ctt ggt ggt ttg ttt tcc aag aag tgg aag   640
Glu Lys Leu Leu Gly Asp Leu Gly Gly Leu Phe Ser Lys Lys Trp Lys
             175   180   185

```
cca aag aag aac ggc gca atc agg ggc cct atg ctg acc aga gac gat   688
Pro Lys Lys Asn Gly Ala Ile Arg Gly Pro Met Leu Thr Arg Asp Asp
        190                 195                 200

tcc ttc ata cgc aag ggc agc cat atg gag cag agg cat aaa ctg ggg   736
Ser Phe Ile Arg Lys Gly Ser His Met Glu Gln Arg His Lys Leu Gly
    205                 210                 215

ctg tca gat cgt ccg cat cga tcc aat gca cgc cag ttc cta tct gaa   784
Leu Ser Asp Arg Pro His Arg Ser Asn Ala Arg Gln Phe Leu Ser Glu
220                 225                 230                 235

ccc aca tca ggc ctt gag aaa gtc gag gtg gag aag gca aag cag gat   832
Pro Thr Ser Gly Leu Glu Lys Val Glu Val Glu Lys Ala Lys Gln Asp
                240                 245                 250

gat ggc ctg tct gac ctt agc gac ata ctg aca gag ttg aaa gga atg   880
Asp Gly Leu Ser Asp Leu Ser Asp Ile Leu Thr Glu Leu Lys Gly Met
                255                 260                 265

gcc att gac atg gga act gag att gag ggg caa aca aag gat ctt ggt   928
Ala Ile Asp Met Gly Thr Glu Ile Glu Gly Gln Thr Lys Asp Leu Gly
            270                 275                 280

cat gcg gag aag gac ttt gac gaa ctt aac tac agg gtc aag ggg gca   976
His Ala Glu Lys Asp Phe Asp Glu Leu Asn Tyr Arg Val Lys Gly Ala
    285                 290                 295

aac gct cga aca cgt cgc ctg ctt ggc aga taggcaagaa gcatatgttg   1026
Asn Ala Arg Thr Arg Arg Leu Leu Gly Arg
300                 305

ttcaccagag gattctgtga cactccttat cttctgcatt tgctttcgtg ggctgttaat 1086

tcagatcatt ttgtgcataa aactctggtt aggaaggtct gttggggagt tgtatcaggg 1146

tttattgtgt atatacgcta gacgggcggt tcgttttcta tgttgcagtt gtactacatt 1206

tgctatggac agtagatacg tttgtattcg gttttcttgt tttgcaatcg ctatgctgca 1266

ggaaagcac                                                        1275
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<210> 44
<211> 309
<212> PRT
<213> Hordeum vulgare

<400> 44
Met Ser Ala Thr Arg Pro Ser Phe Phe Pro Ser Asn Asn Asn Arg Asn
  1               5                  10                  15

Lys Pro Ala Thr Arg Asn Pro Phe Asp Ser Asp Ser Asp Asp Asp Gly
            20                  25                  30

Gly Met Ala Arg Arg Gly Pro Ala Arg Ala Ser Ser Val Pro Thr Pro
        35                  40                  45
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Ala Ala Gly Pro Ala Arg Ala Ser Ser Ala Pro Ile Pro Ala Asp Glu
    50              55              60

Ala Asp Gln Arg Gly Ala Leu Phe Gly Ala Gly Pro Ala Pro Ser Gly
65              70              75                      80

Phe Ala Ser Ser Ser Ser Ala Ala Ala Arg Gly Arg Tyr Arg Asn Asp
            85              90                      95

Phe Arg Asp Ser Gly Gly Val Glu Ala Gln Ser Val Gln Glu Leu Glu
            100             105             110

Gly Tyr Ala Ala Tyr Lys Ala Glu Glu Thr Thr Arg Arg Val Asp Gly
        115             120             125

Cys Leu Arg Val Ala Glu Glu Met Arg Asp Thr Ala Ser Lys Thr Leu
    130             135             140

Leu Gln Val His Gln Gln Gly Gln Gln Ile Arg Arg Thr His Ala Met
145             150             155             160

Ala Val Asp Ile Asp Gln Asp Leu Ser Arg Gly Glu Lys Leu Leu Gly
            165             170             175

Asp Leu Gly Gly Leu Phe Ser Lys Lys Trp Lys Pro Lys Lys Asn Gly
            180             185             190

Ala Ile Arg Gly Pro Met Leu Thr Arg Asp Asp Ser Phe Ile Arg Lys
        195             200             205

Gly Ser His Met Glu Gln Arg His Lys Leu Gly Leu Ser Asp Arg Pro
    210             215             220

His Arg Ser Asn Ala Arg Gln Phe Leu Ser Glu Pro Thr Ser Gly Leu
225             230             235             240

Glu Lys Val Glu Val Glu Lys Ala Lys Gln Asp Asp Gly Leu Ser Asp
            245             250             255

Leu Ser Asp Ile Leu Thr Glu Leu Lys Gly Met Ala Ile Asp Met Gly
            260             265             270

Thr Glu Ile Glu Gly Gln Thr Lys Asp Leu Gly His Ala Glu Lys Asp
        275             280             285

Phe Asp Glu Leu Asn Tyr Arg Val Lys Gly Ala Asn Ala Arg Thr Arg
    290             295             300

Arg Leu Leu Gly Arg
305
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<213> Consensus

<220>
<221> misc_feature
<222> (2)..(2)
<223> l or i

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 45
His Leu Lys Xaa Val Tyr
1   5

<210> 46
<211> 7
<212> PRT
<213> Consensus

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> y or f

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 46
Ala Xaa Gly Ala Tyr Xaa His
1   5

<210> 47
<211> 4
<212> PRT
<213> Consensus

<400> 47

Asn Ile Gly Gly
1

<210> 48
<211> 8
<212> PRT
<213> Consensus

<220>
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<222> (2)..(2)
<223> v or p

<220>
<221> misc_feature
<222> (3)..(3)
<223> y or f

<220>
<221> misc_feature
<222> (5)..(5)
<223> e or q

<220>
<221> misc_feature
<222> (6)..(6)
<223> r or q

<400> 48
Pro Val Tyr Glu Glu Arg Lys Arg
1   5

<210> 49
<211> 8
<212> PRT
<213> Consensus

<220>
<221> misc_feature
<222> (1)..(1)
<223> e or q

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or s

<220>
<221> misc_feature
<222> (5)..(5)
<223> v or i

<400> 49
Glu Gly Ala Ser Val Gly Pro Leu
1   5

<210> 50
<211> 5
<212> PRT
<213> Consensus

<220>

<221> misc_feature
<222> (3)..(3)
<223> s or g

<220>
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<222> (4)..(4)
<223> l or i

<220>
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<222> (5)..(5)
<223> i or l

<400> 50
Asp Pro Ser Leu Ile
1   5

<210> 51
<211> 11
<212> PRT
<213> Consensus

<220>
<221> misc_feature
<222> (2)..(2)
<223> g or a

<220>
<221> misc_feature
<222> (4)..(4)
<223> a or s

<220>
<221> misc_feature
<222> (5)..(5)
<223> l or i

<220>
<221> misc_feature
<222> (8)..(8)
<223> a or g

<220>
<221> misc_feature
<222> (11)..(11)
<223> s or t

<400> 51
Val Gly Thr Ala Leu Ala Phe Ala Cys Phe Ser
1   5   10

<210> 52
<211> 6
<212> PRT

<213>   Consensus

<220>
<221>   misc_feature
<222>   (3)..(3)
<223>   y or f

<400>   52
Tyr Leu Tyr Leu Gly Gly
1   5

<210>   53
<211>   7
<212>   PRT
<213>   Consensus

<400>   53
Glu Tyr Leu Tyr Leu Gly Gly
1   5

<210>   54
<211>   11
<212>   PRT
<213>   Consensus

<220>
<221>   misc_feature
<222>   (2)..(2)
<223>   l or v

<220>
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<223>   g or w

<220>
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<222>   (7)..(7)
<223>   s or t

<220>
<221>   misc_feature
<222>   (8)..(8)
<223>   i or m

<220>
<221>   misc_feature
<222>   (10)..(10)
<223>   l or m

<400>   54
Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp
1   5   10

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<210>  55
<211>  7
<212>  PRT
<213>  Consensus

<220>
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<222>  (4)..(4)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  i or v

<220>
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<222>  (6)..(6)
<223>  i or v

<400>  55
Asp Thr Gly Xaa Ile Ile Glu
1                   5


<210>  56
<211>  24
<212>  DNA
<213>  Artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(24)
<223>  BI1-sense primer

<400>  56
atggacgcct tctactcgac ctcg                                      24


<210>  57
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(20)
<223>  BI1-antisense primer

<400>  57
gccagagcag gatcgacgcc                                           20


<210>  58
<211>  21
<212>  DNA
<213>  Artificial sequence
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<220>
<221>  misc_feature
<222>  (1)..(21)
<223>  UBI-sense primer

<400>  58
ccaagatgca gatcttcgtg a                                      21


<210>  59
<211>  21
<212>  DNA
<213>  Artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(21)
<223>  UBI-antisense primer

<400>  59
ttcgcgatag gtaaaagagc a                                      21


<210>  60
<211>  26
<212>  DNA
<213>  Artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(26)
<223>  BI1VL sense primer

<400>  60
ggattcaacg cgagcgcagg acaagc                                 26


<210>  61
<211>  26
<212>  DNA
<213>  Artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(26)
<223>  BI1VL antisense primer

<400>  61
gtcgacgcgg tgacggtatc tacatg                                 26


<210>  62
<211>  18
<212>  DNA
<213>  Artificial sequence
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<220>
<221>  misc_feature
<222>  (1)..(18)
<223>  M13-fwd primer

<400>  62
gtaaaacgac ggccagtg                                              18


<210>  63
<211>  19
<212>  DNA
<213>  Artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(19)
<223>  M13-rev primer

<400>  63
ggaaacagct atgaccatg                                             19
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